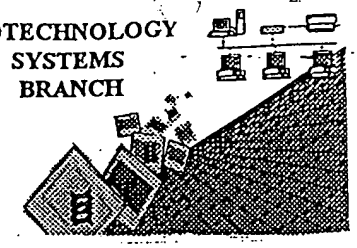
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BIOTECHNOLOGY SYSTEMS BRANCH



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1645

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Error on p. 5

Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
Output Set: N:\CRF3\06172002\I378045C.raw

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 3 <110> APPLICANT: Rauch, Charles
 4       Walczak, Henning
 6 <120> TITLE OF INVENTION: RECEPTOR THAT BINDS TRAIL
 8 <130> FILE REFERENCE: 2625-E
10 <140> CURRENT APPLICATION NUMBER: US 09/378,045C
11 <141> CURRENT FILING DATE: 1999-08-20
13 <150> PRIOR APPLICATION NUMBER: US 08/883,036
14 <151> PRIOR FILING DATE: 1997-06-26
16 <150> PRIOR APPLICATION NUMBER: US 08/869,852
17 <151> PRIOR FILING DATE: 1997-06-04
19 <150> PRIOR APPLICATION NUMBER: US 08/829,536
20 <151> PRIOR FILING DATE: 1997-03-28
22 <150> PRIOR APPLICATION NUMBER: US 08/815,255
23 <151> PRIOR FILING DATE: 1997-03-12
25 <150> PRIOR APPLICATION NUMBER: US 08/799,861
26 <151> PRIOR FILING DATE: 1997-02-13
28 <160> NUMBER OF SEQ ID NOS: 6
30 <170> SOFTWARE: PatentIn version 3.1
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 1323
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (1)..(1323)
40 <223> OTHER INFORMATION:
43 <400> SEQUENCE: 1
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45 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
46 1               5                  10                  15
48 agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ccc       96
49 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
50             20                  25                  30
52 cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg      144
53 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
54         35                  40                  45
56 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag      192
57 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
58     50                  55                  60
60 cag aga gcg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg      240
61 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
62 65                  70                  75                  80
64 tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc      288
```

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65 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
66                 85                  90                  95
68 tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc      336
69 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
70             100                 105                 110
72 tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccg      384
73 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
74         115                 120                 125
76 tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc      432
77 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
78     130                 135                 140
80 cgg gaa gaa gat tct cct gag atg tgc cgg aag tgc cgc aca ggg tgt      480
81 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
82 145                 150                 155                 160
84 ccc aga ggg atg gtc aag gtc ggt gat tgt aca ccc tgg agt gac atc      528
85 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
86                 165                 170                 175
88 gaa tgt gtc cac aaa gaa tca ggt aca aag cac agt ggg gaa gcc cca      576
89 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
90             180                 185                 190
92 gct gtg gag gag acg gtg acc tcc agc cca ggg act cct gcc tct ccc      624
93 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
94         195                 200                 205
96 tgt tct ctc tca ggc atc atc ata gga gtc aca gtt gca gcc gta gtc      672
97 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
98     210                 215                 220
100 ttg att gtg gct gtg ttt gtt tgc aag tct tta ctg tgg aag aaa gtc      720
101 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
102 225                 230                 235                 240
104 ctt cct tac ctg aaa ggc atc tgc tca ggt ggt ggt ggg gac cct gag      768
105 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
106                 245                 250                 255
108 cgt gtg gac aga agc tca caa cga cct ggg gct gag gac aat gtc ctc      816
109 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
110             260                 265                 270
112 aat gag atc gtg agt atc ttg cag ccc acc cag gtc cct gag cag gaa      864
113 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
114         275                 280                 285
116 atg gaa gtc cag gag cca gca gag cca aca ggt gtc aac atg ttg tcc      912
117 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
118     290                 295                 300
120 ccc ggg gag tca gag cat ctg ctg gaa ccg gca gaa gct gaa agg tct      960
121 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
122 305                 310                 315                 320
124 cag agg agg agg ctg ctg gtt cca gca aat gaa ggt gat ccc act gag     1008
125 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
126                 325                 330                 335
128 act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc ttt gac     1056
129 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
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Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
Output Set: N:\CRF3\06172002\I378045C.raw

```
130                340                 345                 350
132 tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat gag ata     1104
133 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
134         355                 360                 365
136 aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg tac acg     1152
137 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
138     370                 375                 380
140 atg ctg ata aag tgg gtc aac aaa acc ggg cga gat gcc tct gtc cac     1200
141 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
142 385                 390                 395                 400
144 acc ctg ctg gat gcc ttg gag acg ctg gga gag aga ctt gcc aag cag     1248
145 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
146                 405                 410                 415
148 aag att gag gac cac ttg ttg agc tct gga aag ttc atg tat cta gaa     1296
149 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
150                 420                 425                 430
152 ggt aat gca gac tct gcc atg tcc taa                                1323
153 Gly Asn Ala Asp Ser Ala Met Ser
154         435                 440
157 <210> SEQ ID NO: 2
158 <211> LENGTH: 440
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 2
164 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
165 1               5                   10                  15
168 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Pro
169             20                  25                  30
172 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
173         35                  40                  45
176 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
177     50                  55                  60
180 Gln Arg Ala Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
181 65                  70                  75                  80
184 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
185                 85                  90                  95
188 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
189             100                 105                 110
192 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
193         115                 120                 125
196 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
197     130                 135                 140
200 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
201 145                 150                 155                 160
204 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
205                 165                 170                 175
208 Glu Cys Val His Lys Glu Ser Gly Thr Lys His Ser Gly Glu Ala Pro
209             180                 185                 190
212 Ala Val Glu Glu Thr Val Thr Ser Ser Pro Gly Thr Pro Ala Ser Pro
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Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
Output Set: N:\CRF3\06172002\I378045C.raw

```
213         195                 200                 205
216 Cys Ser Leu Ser Gly Ile Ile Ile Gly Val Thr Val Ala Ala Val Val
217     210                 215                 220
220 Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp Lys Lys Val
221 225                 230                 235                 240
224 Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly Gly Asp Pro Glu
225                 245                 250                 255
228 Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp Asn Val Leu
229             260                 265                 270
232 Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro Glu Gln Glu
233         275                 280                 285
236 Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn Met Leu Ser
237     290                 295                 300
240 Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala Glu Arg Ser
241 305                 310                 315                 320
244 Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp Pro Thr Glu
245                 325                 330                 335
248 Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe Asp
249             340                 345                 350
252 Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu Ile
253         355                 360                 365
256 Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Tyr Thr
257     370                 375                 380
260 Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala Ser Val His
261 385                 390                 395                 400
264 Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu Ala Lys Gln
265                 405                 410                 415
268 Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met Tyr Leu Glu
269             420                 425                 430
272 Gly Asn Ala Asp Ser Ala Met Ser
273         435                 440
276 <210> SEQ ID NO: 3
277 <211> LENGTH: 157
278 <212> TYPE: DNA
279 <213> ORGANISM: Homo sapiens
281 <220> FEATURE:
282 <221> NAME/KEY: CDS
283 <222> LOCATION: (3)..(155)
284 <223> OTHER INFORMATION:
287 <220> FEATURE:
288 <221> NAME/KEY: misc_feature
289 <222> LOCATION: (145)..(145)
290 <223> OTHER INFORMATION: "n" = a, t, g, or c
293 <220> FEATURE:
294 <221> NAME/KEY: misc_feature
295 <222> LOCATION: (149)..(149)
296 <223> OTHER INFORMATION: "n" = a, t, g, or c
299 <400> SEQUENCE: 3
300 ct gag act ctg aga cag tgc ttc gat gac ttt gca gac ttg gtg ccc        47
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Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
Output Set: N:\CRF3\06172002\I378045C.raw

```
301    Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro
302    1               5                  10                  15
304 ttt gac tcc tgg gag ccg ctc atg agg aag ttg ggc ctc atg gac aat       95
305 Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn
306                 20                  25                  30
308 gag ata aag gtg gct aaa gct gag gca gcg ggc cac agg gac acc ttg      143
309 Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu
310             35                  40                  45
W--> 312 tnc acn atg ctg at                                           157
W--> 313 Xaa Xaa Met Leu
314         50
317 <210> SEQ ID NO: 4
318 <211> LENGTH: 51
319 <212> TYPE: PRT
320 <213> ORGANISM: Homo sapiens
322 <220> FEATURE:
323 <221> NAME/KEY: misc_feature
324 <222> LOCATION: (48)..(48)
325 <223> OTHER INFORMATION: The 'Xaa' at location 48 stands for Tyr, Cys, Ser, or Phe.
327 <220> FEATURE:
328 <221> NAME/KEY: misc_feature
329 <222> LOCATION: (49)..(49)
330 <223> OTHER INFORMATION: The 'Xaa' at location 49 stands for Thr.
332 <220> FEATURE:
333 <221> NAME/KEY: misc_feature
334 <222> LOCATION: (145)..(145)
335 <223> OTHER INFORMATION: "n" = a, t, g, or c
337 <220> FEATURE:
338 <221> NAME/KEY: misc_feature
339 <222> LOCATION: (149)..(149)
340 <223> OTHER INFORMATION: "n" = a, t, g, or c
342 <400> SEQUENCE: 4
344 Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val Pro Phe
345 1               5                  10                  15
348 Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp Asn Glu
349             20                  25                  30
W--> 352 Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr Leu Xaa
353         35                  40                  45
W--> 356 Xaa Met Leu
357     50
360 <210> SEQ ID NO: 5
361 <211> LENGTH: 8
362 <212> TYPE: PRT
363 <213> ORGANISM: Artificial Sequence
365 <220> FEATURE:
366 <223> OTHER INFORMATION: FLAG peptide
368 <400> SEQUENCE: 5
370 Asp Tyr Lys Asp Asp Asp Asp Lys
371 1               5
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no positions 145 + 149 -
no Ns in a protein sequence!

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 06/17/2002
PATENT APPLICATION: US/09/378,045C TIME: 14:53:33

Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 145,149
Seq#:3; Xaa Pos. 48,49
Seq#:4; Xaa Pos. 48,49

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VERIFICATION SUMMARY DATE: 06/17/2002
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Input Set : A:\2625-Erevsd seqlist as filed 010702.txt
Output Set: N:\CRF3\06172002\I378045C.raw

L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:143
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:157
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:32
L:356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:48

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